

OIPF #6

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/728,420A

DATE: 08/14/2001
 TIME: 08:49:14

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3 <110> APPLICANT: Yoshinaga, Steven
4   Mak, Tak
5   Shahinian, Arda
6   Trafuri Blatt, Anna
7   Senaldi, Giorgio
9 <120> TITLE OF INVENTION: Polypeptides Involved in Immune Response
11 <130> FILE REFERENCE: A-579C
13 <140> CURRENT APPLICATION NUMBER: 09/728,420A
14 <141> CURRENT FILING DATE: 2000-11-28
16 <150> PRIOR APPLICATION NUMBER: PCT/US00/01871
17 <151> PRIOR FILING DATE: 2000-01-27
19 <150> PRIOR APPLICATION NUMBER: US 09/264,527
20 <151> PRIOR FILING DATE: 1999-03-08
22 <150> PRIOR APPLICATION NUMBER: US 09/244,448
23 <151> PRIOR FILING DATE: 1999-02-03
25 <160> NUMBER OF SEQ ID NOS: 35
27 <170> SOFTWARE: PatentIn version 3.0
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31 <212> TYPE: DNA
32 <213> ORGANISM: Mus musculus
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35 <221> NAME/KEY: CDS
36 <222> LOCATION: (1)..(600)
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43 ctt tta aca gga gaa atc aat ggc tcg gcc gat cat agg atg ttt tca      96
44 Leu Leu Thr Gly Glu Ile Asn Gly Ser Ala Asp His Arg Met Phe Ser
45 20 25 30
47 ttt cac aat gga ggt gta cag att tct tgt aaa tac cct gag act gtc      144
48 Phe His Asn Gly Gly Val Gln Ile Ser Cys Lys Tyr Pro Glu Thr Val
49 35 40 45
51 cag cag tta aaa atg cga ttg ttc aga gag aga gaa gtc ctc tgc gaa      192
52 Gln Gln Leu Lys Met Arg Leu Phe Arg Glu Arg Glu Val Leu Cys Glu
53 50 55 60
55 ctc acc aag acc aag gga agc gga aat gcg gtg tcc atc aag aat cca      240
56 Leu Thr Lys Thr Lys Gly Ser Gly Asn Ala Val Ser Ile Lys Asn Pro
57 65 70 75 80
59 atg ctc tgt cta tat cat ctg tca aac aac agc gtc tct ttt ttc cta      288
60 Met Leu Cys Leu Tyr His Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
61 85 90 95
63 aac aac cca gac agc tcc cag gga agc tat tac ttc tgc agc ctg tcc      336
64 Asn Asn Pro Asp Ser Ser Gln Gly Ser Tyr Tyr Phe Cys Ser Leu Ser
65 100 105 110
67 att ttt gac cca cct cct ttt caa gaa agg aac ctt agt gga gga tat      384

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68 Ile Phe Asp Pro Pro Pro Phe Gln Glu Arg Asn Leu Ser Gly Gly Tyr
69          115          120          125
71 ttg cat att tat gaa tcc cag ctc tgc tgc cag ctg aag ctc tgg cta      432
72 Leu His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu
73          130          135          140
75 ccc gta ggg tgt gca gct ttc gtt gtg gta ctc ctt ttt gga tgc ata      480
76 Pro Val Gly Cys Ala Ala Phe Val Val Val Leu Leu Phe Gly Cys Ile
77 145          150          155          160
79 ctt atc atc tgg ttt tca aaa aag aaa tac gga tcc agt gtg cat gac      528
80 Leu Ile Ile Trp Phe Ser Lys Lys Lys Tyr Gly Ser Ser Val His Asp
81          165          170          175
83 cct aat agt gaa tac atg ttc atg gcg gca gtc aac aca aac aaa aag      576
84 Pro Asn Ser Glu Tyr Met Phe Met Ala Ala Val Asn Thr Asn Lys Lys
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103 Leu Leu Thr Gly Glu Ile Asn Gly Ser Ala Asp His Arg Met Phe Ser
104          20          25          30
107 Phe His Asn Gly Gly Val Gln Ile Ser Cys Lys Tyr Pro Glu Thr Val
108          35          40          45
111 Gln Gln Leu Lys Met Arg Leu Phe Arg Glu Arg Glu Val Leu Cys Glu
112          50          55          60
115 Leu Thr Lys Thr Lys Gly Ser Gly Asn Ala Val Ser Ile Lys Asn Pro
116 65          70          75          80
119 Met Leu Cys Leu Tyr His Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
120          85          90          95
123 Asn Asn Pro Asp Ser Ser Gln Gly Ser Tyr Tyr Phe Cys Ser Leu Ser
124          100          105          110
127 Ile Phe Asp Pro Pro Pro Phe Gln Glu Arg Asn Leu Ser Gly Gly Tyr
128          115          120          125
131 Leu His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu
132          130          135          140
135 Pro Val Gly Cys Ala Ala Phe Val Val Val Leu Leu Phe Gly Cys Ile
136 145          150          155          160
139 Leu Ile Ile Trp Phe Ser Lys Lys Lys Tyr Gly Ser Ser Val His Asp
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147 Ser Arg Leu Ala Gly Val Thr Ser
148          195          200
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162 20 25 30
164 Phe His Asn Gly Gly Val Gln Ile Ser Cys Lys Tyr Pro Glu Thr Val
165 35 40 45
167 Gln Gln Leu Lys Met Arg Leu Phe Arg Glu Arg Glu Val Leu Cys Glu
168 50 55 60
170 Leu Thr Lys Thr Lys Gly Ser Gly Asn Ala Val Ser Ile Lys Asn Pro
171 65 70 75 80
173 Met Leu Cys Leu Tyr His Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
174 85 90 95
176 Asn Asn Pro Asp Ser Ser Gln Gly Ser Tyr Tyr Phe Cys Ser Leu Ser
177 100 105 110
179 Ile Phe Asp Pro Pro Pro Phe Gln Glu Arg Asn Leu Ser Gly Gly Tyr
180 115 120 125
182 Leu His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu
183 130 135 140
185 Pro Val Gly Cys Ala Ala Phe Val Val Val Leu Leu Phe Gly Cys Ile
186 145 150 155 160
188 Leu Ile Ile Trp Phe Ser Lys Lys Lys Tyr Gly Ser Ser Val His Asp
189 165 170 175
191 Pro Asn Ser Glu Tyr Met Phe Met Ala Ala Val Asn Thr Asn Lys Lys
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199 <212> TYPE: PRT
200 <213> ORGANISM: Mus musculus
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205 1 5 10 15
207 Val Thr Glu Asn Lys Ile Leu Val Lys Gln Ser Pro Leu Leu Val Val
208 20 25 30
210 Asp Ser Asn Glu Val Ser Leu Ser Cys Arg Tyr Ser Tyr Asn Leu Leu
211 35 40 45
213 Ala Lys Glu Phe Arg Ala Ser Leu Tyr Lys Gly Val Asn Ser Asp Val
214 50 55 60
216 Glu Val Cys Val Gly Asn Gly Asn Phe Thr Tyr Gln Pro Gln Phe Arg
217 65 70 75 80
219 Ser Asn Ala Glu Phe Asn Cys Asp Gly Asp Phe Asp Asn Glu Thr Val
220 85 90 95
222 Thr Phe Arg Leu Trp Asn Leu His Val Asn His Thr Asp Ile Tyr Phe
223 100 105 110

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225 Cys Lys Ile Glu Phe Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Arg
226      115      120      125
228 Ser Asn Gly Thr Ile Ile His Ile Lys Glu Lys His Leu Cys His Thr
229      130      135      140
231 Gln Ser Ser Pro Lys Leu Phe Trp Ala Leu Val Val Val Ala Gly Val
232 145      150      155      160
234 Leu Phe Cys Tyr Gly Leu Leu Val Thr Val Ala Leu Cys Val Ile Trp
235      165      170      175
237 Thr Asn Ser Arg Arg Asn Arg Leu Leu Gln Val Thr Thr Met Asn Met
238      180      185      190
240 Thr Pro Arg Arg Pro Gly Leu Thr Arg Lys Pro Tyr Gln Pro Tyr Ala
241      195      200      205
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244      210      215
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247 <211> LENGTH: 44
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249 <213> ORGANISM: Artificial sequence
251 <220> FEATURE:
252 <221> NAME/KEY: misc_feature
253 <223> OTHER INFORMATION: Synthetic
256 <400> SEQUENCE: 5
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259 1      5      10      15
261 Asn Tyr Phe Cys Pro Pro Pro Ser Gly His Ile Glu Leu Cys Lys Leu
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264 Trp Leu Val Phe Leu Leu Leu Ile Trp Pro Arg Ala
265      35      40
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274 <222> LOCATION: (1)..(966)
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279 1      5      10      15
281 gtt tgg aag aag ctc cat gtt tct agc ggg ttc ttt tct ggt ctt ggt      96
282 Val Trp Lys Lys Leu His Val Ser Ser Gly Phe Phe Ser Gly Leu Gly      30
283      20      25      30
285 ctg ttc ttg ctg ctg ttg agc agc ctc tgt gct gcc tct gca gag act      144
286 Leu Phe Leu Leu Leu Leu Ser Ser Leu Cys Ala Ala Ser Ala Glu Thr      45
287      35      40      45
289 gaa gtc ggt gca atg gtg ggc agc aat gtg gtg ctc agc tgc att gac      192
290 Glu Val Gly Ala Met Val Gly Ser Asn Val Val Leu Ser Cys Ile Asp      60
291      50      55      60
293 ccc cac aga cgc cat ttc aac ttg agt ggt ctg tat gtc tat tgg caa      240

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297	atc	gaa	aac	cca	gaa	gtt	tcg	gtg	act	tac	tac	ctg	cct	tac	aag	tct	288
298	Ile	Glu	Asn	Pro	Glu	Val	Ser	Val	Thr	Tyr	Tyr	Leu	Pro	Tyr	Lys	Ser	
299					85					90					95		
301	cca	ggg	atc	aat	gtg	gac	agt	tcc	tac	aag	aac	agg	ggc	cat	ctg	tcc	336
302	Pro	Gly	Ile	Asn	Val	Asp	Ser	Ser	Tyr	Lys	Asn	Arg	Gly	His	Leu	Ser	
303				100					105					110			
305	ctg	gac	tcc	atg	aag	cag	ggt	aac	ttc	tct	ctg	tac	ctg	aag	aat	gtc	384
306	Leu	Asp	Ser	Met	Lys	Gln	Gly	Asn	Phe	Ser	Leu	Tyr	Leu	Lys	Asn	Val	
307			115					120					125				
309	acc	cct	cag	gat	acc	cag	gag	ttc	aca	tgc	cgg	gta	ttt	atg	aat	aca	432
310	Thr	Pro	Gln	Asp	Thr	Gln	Glu	Phe	Thr	Cys	Arg	Val	Phe	Met	Asn	Thr	
311		130				135						140					
313	gcc	aca	gag	tta	gtc	aag	atc	ttg	gaa	gag	gtg	gtc	agg	ctg	cgt	gtg	480
314	Ala	Thr	Glu	Leu	Val	Lys	Ile	Leu	Glu	Glu	Val	Val	Arg	Leu	Arg	Val	
315	145				150					155					160		
317	gca	gca	aac	ttc	agt	aca	cct	gtc	atc	agc	acc	tct	gat	agc	tcc	aac	528
318	Ala	Ala	Asn	Phe	Ser	Thr	Pro	Val	Ile	Ser	Thr	Ser	Asp	Ser	Ser	Asn	
319				165					170					175			
321	ccg	ggc	cag	gaa	cgt	acc	tac	acc	tgc	atg	tcc	aag	aat	ggc	tac	cca	576
322	Pro	Gly	Gln	Glu	Arg	Thr	Tyr	Thr	Cys	Met	Ser	Lys	Asn	Gly	Tyr	Pro	
323			180					185					190				
325	gag	ccc	aac	ctg	tat	tgg	atc	aac	aca	acg	gac	aat	agc	cta	ata	gac	624
326	Glu	Pro	Asn	Leu	Tyr	Trp	Ile	Asn	Thr	Thr	Asp	Asn	Ser	Leu	Ile	Asp	
327		195				200						205					
329	acg	gct	ctg	cag	aat	aac	act	gtc	tac	ttg	aac	aag	ttg	ggc	ctg	tat	672
330	Thr	Ala	Leu	Gln	Asn	Asn	Thr	Val	Tyr	Leu	Asn	Lys	Leu	Gly	Leu	Tyr	
331		210				215					220						
333	gat	gta	atc	agc	aca	tta	agg	ctc	cct	tgg	aca	tct	cgt	ggg	gat	gtt	720
334	Asp	Val	Ile	Ser	Thr	Leu	Arg	Leu	Pro	Trp	Thr	Ser	Arg	Gly	Asp	Val	
335	225				230					235				240			
337	ctg	tgc	tgc	gta	gag	aat	gtg	gct	ctc	cac	cag	aac	atc	act	agc	att	768
338	Leu	Cys	Cys	Val	Glu	Asn	Val	Ala	Leu	His	Gln	Asn	Ile	Thr	Ser	Ile	
339				245					250				255				
341	agc	cag	gca	gaa	agt	ttc	act	gga	aat	aac	aca	aag	aac	cca	cag	gaa	816
342	Ser	Gln	Ala	Glu	Ser	Phe	Thr	Gly	Asn	Asn	Thr	Lys	Asn	Pro	Gln	Glu	
343			260					265					270				
345	acc	cac	aat	aat	gag	tta	aaa	gtc	ctt	gtc	ccc	gtc	ctt	gct	gta	ctg	864
346	Thr	His	Asn	Asn	Glu	Leu	Lys	Val	Leu	Val	Pro	Val	Leu	Ala	Val	Leu	
347			275				280					285					
349	gcg	gca	gcg	gca	ttc	gtt	tcc	ttc	atc	ata	tac	aga	cgc	acg	cgt	ccc	912
350	Ala	Ala	Ala	Ala	Phe	Val	Ser	Phe	Ile	Ile	Tyr	Arg	Arg	Thr	Arg	Pro	
351		290				295					300						
353	cac	cga	agc	tat	aca	gga	ccc	aag	act	gta	cag	ctt	gaa	ctt	aca	gac	960
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355	305				310					315				320			
357	cac	gcc															966
358	His	Ala															

VERIFICATION SUMMARY

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